

THAT WHICH IS CLAIMED:

Def a3

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1. An isolated nucleotide molecule comprising a nucleotide sequence selected from the group consisting of:
- (a) a nucleotide sequence set forth in SEQ ID NO: 1;
  - (b) a nucleotide sequence set forth in SEQ ID NO: 2;
  - (c) a nucleotide sequence set forth in SEQ ID NO: 3;
  - (d) a nucleotide sequence set forth in SEQ ID NO: 7;
  - (e) a nucleotide sequence set forth in SEQ ID NO: 8;
  - 10 (f) a nucleotide sequence consisting of at least 19 contiguous nucleotides of the nucleotide sequence set forth in any one of (a)-(e);
  - (h) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 9;
  - (i) a nucleotide sequence encoding at least 70 contiguous amino acids
  - 15 of the amino acid sequence set forth in SEQ ID NO: 9;
  - (j) a nucleotide sequence comprising at least 80% identity to the sequence set forth in SEQ ID NO: 7;
  - (k) a nucleotide sequence comprising at least 80% identity to the sequence set forth in SEQ ID NO: 8;
  - 20 (l) a nucleotide sequence that is complementary to the nucleotide sequence of any one of (a)-(k); and
  - (m) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence any one of (a)-(e), or to a complementary sequence thereof.
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2. An expression cassette comprising the nucleotide sequence of claim 1, said nucleotide sequence operably linked to a promoter that drives expression in a plant cell.
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3. The expression cassette of claim 2, wherein said promoter is selected from the group consisting of tissue-preferred, constitutive, chemically regulatable, and pathogen-preferred promoters.

4. A transformed plant having stably incorporated into its genome a nucleotide sequence operably linked to a promoter that drives expression in a plant cell, wherein said nucleotide sequence is selected from the group consisting of:

- 5 (a) a nucleotide sequence set forth in SEQ ID NO: 1;
- (b) a nucleotide sequence set forth in SEQ ID NO: 2;
- (c) a nucleotide sequence set forth in SEQ ID NO: 3;
- (d) a nucleotide sequence set forth in SEQ ID NO: 7;
- (e) a nucleotide sequence set forth in SEQ ID NO: 8;
- 10 (f) a nucleotide sequence consisting of at least 19 contiguous nucleotides of the nucleotide sequence set forth in any one of (a)-(e);
- (h) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 9;
- (i) a nucleotide sequence encoding at least 70 contiguous amino acids
- 15 of the amino acid sequence set forth in SEQ ID NO: 9;
- (j) a nucleotide sequence comprising at least 80% identity to the sequence set forth in SEQ ID NO: 7;
- (k) a nucleotide sequence comprising at least 80% identity to the sequence set forth in SEQ ID NO: 8;
- 20 (l) a nucleotide sequence that is complementary to the nucleotide sequence of any one of (a)-(k); and
- (m) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence any one of (a)-(e), or to a complementary sequence thereof.

25 5. The plant of claim 4, wherein said promoter is selected from the group consisting of tissue-preferred, constitutive, chemically regulatable, and pathogen-preferred promoters.

30 6. The plant of claim 4, wherein said nucleotide sequence is operably linked to said promoter for the production of antisense transcripts.

7. The plant of claim 4, wherein said plant is a monocot.

8. The plant of claim 7, wherein said monocot is selected from the group consisting of maize, wheat, rice, Basmati rice, sorghum, rye, millet and barley.

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9. The plant of claim 4, wherein said plant is a dicot.

*Ant*  
10 fruit trees.  
10 The plant of claim 9, wherein said dicot is selected from the group consisting of soybeans, sunflowers, safflowers, alfalfa, Brassica sp., cotton, peanuts and

11. Transformed seed of the plant of claim 4.

12. Transformed seed of the plant of claim 5.

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13. Transformed seed of the plant of claim 6.

14. Transformed seed of the plant of claim 7.

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15. Transformed seed of the plant of claim 8.

16. Transformed seed of the plant of claim 9.

17. Transformed seed of the plant of claim 10.

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*Ant*  
18. A method for modifying the growth of an organism, said method comprising transforming an organism with a nucleotide sequence encoding a P-glycoprotein wherein said P-glycoprotein functions to control growth of an organism, said nucleotide sequence operably linked to a promoter capable of driving the expression  
30 of said sequence in said organism.

19. The method of claim 18, wherein said organism is a plant and said nucleotide sequence is selected from the group consisting of:

- 5 (a) a nucleotide sequence set forth in SEQ ID NO: 1;  
(b) a nucleotide sequence set forth in SEQ ID NO: 2;  
(c) a nucleotide sequence set forth in SEQ ID NO: 3;  
(d) a nucleotide sequence set forth in SEQ ID NO: 7;  
(e) a nucleotide sequence set forth in SEQ ID NO: 8;  
(f) a nucleotide sequence consisting of at least 19 contiguous nucleotides of the nucleotide sequence set forth in any one of (a)-(e);  
10 (h) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 9;  
(i) a nucleotide sequence encoding at least 70 contiguous amino acids of the amino acid sequence set forth in SEQ ID NO: 9;  
(j) a nucleotide sequence comprising at least 80% identity to the  
15 sequence set forth in SEQ ID NO: 7;  
(k) a nucleotide sequence comprising at least 80% identity to the sequence set forth in SEQ ID NO: 8;  
(l) a nucleotide sequence that is complementary to the nucleotide sequence of any one of (a)-(k); and  
20 (m) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence any one of (a)-(e), or to a complementary sequence thereof.

20. The method of claim 18, wherein said nucleotide sequence is operably linked to said promoter for the production of antisense transcripts.

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21. The method of claim 18, wherein the height of said plant is reduced.

22. The method of claim 18, wherein said plant is a monocot.

30 23. The method of claim 18, wherein said monocot is selected from the group consisting of maize, wheat, rice, Basmati rice, sorghum, rye, millet and barley.

Am 27

24. A transformed plant cell having stably incorporated into its genome a nucleotide sequence operably linked to a promoter that drives expression in a plant cell, wherein said nucleotide sequence is selected from the group consisting of:

- 5 (a) a nucleotide sequence set forth in SEQ ID NO: 1;  
(b) a nucleotide sequence set forth in SEQ ID NO: 2;  
(c) a nucleotide sequence set forth in SEQ ID NO: 3;  
(d) a nucleotide sequence set forth in SEQ ID NO: 7;  
(e) a nucleotide sequence set forth in SEQ ID NO: 8;  
10 (f) a nucleotide sequence consisting of at least 19 contiguous nucleotides of the nucleotide sequence set forth in any one of (a)-(e);  
(h) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 9;  
(i) a nucleotide sequence encoding at least 70 contiguous amino acids  
15 of the amino acid sequence set forth in SEQ ID NO: 9;  
(j) a nucleotide sequence comprising at least 80% identity to the sequence set forth in SEQ ID NO: 7;  
(k) a nucleotide sequence comprising at least 80% identity to the sequence set forth in SEQ ID NO: 8;  
20 (l) a nucleotide sequence that is complementary to the nucleotide sequence of any one of (a)-(k); and  
(m) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence any one of (a)-(e), or to a complementary sequence thereof.

25 25. A method for identifying a plant having a stable mutant phenotype comprising identifying a plant that lacks in its genome at least a portion of an insertion in a gene, wherein: said plant is a descendent of an unstable mutant plant which comprises in its genome an insertion in at least one copy of said gene; and said insertion in said gene is capable of causing said mutant phenotype.

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26. The method of claim 25, wherein said insertion is a duplication or a transposon.

27. The method of claim 25, wherein said phenotype is a dwarf phenotype.

28. The method of claim 25, wherein said gene encodes a P-glycoprotein.

29. The method of claim 28, wherein said plant is sorghum and said gene is *Dw3*.

30. A plant having a stable mutant phenotype according to claim 25.

31. Seed of the plant of claim 30.

32. An isolated protein comprising a member selected from the group consisting of:

(a) a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 9;

(b) a polypeptide comprising at least 70 contiguous amino acids of the amino acid sequence set forth in SEQ ID NO: 9;

(c) a polypeptide encoded by the nucleotide sequence set forth in SEQ ID NO: 8; and

(d) a polypeptide encoded by an amino acid sequence comprising at least 80% identity to the amino sequence of (a).

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